

ATTACHMENT A
(Blast 2 Sequences Results)



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

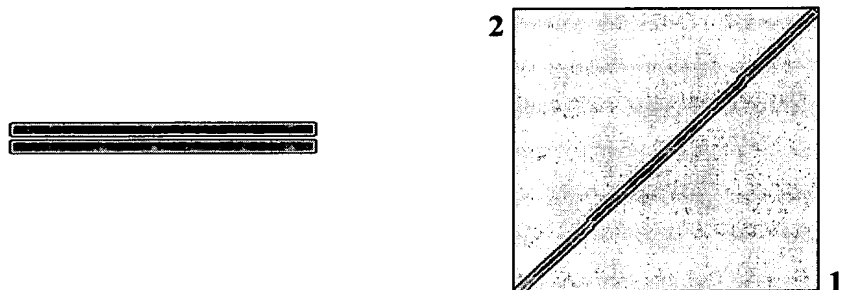
Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.9 [May-01-2004]

Matrix: **BLOSUM62** gap open: **11** gap extension: **1**
 x_dropoff: **50** expect: **10.000** wordsize: **3** Filter ☒ Align

Sequence 1 gi 16324 histone H3.3 like protein [Arabidopsis thaliana] Length 136 (1 .. 136)
 Sequence 2 gi 30315015 histone H3.3 [Vitis vinifera] Length 136 (1 .. 136)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 266 bits (679), Expect = 1e-70
 Identities = 136/136 (100%), Positives = 136/136 (100%)



```

Query:      1  MARTKQTARKSTGGKAPRKQLATKAARKSAPTTGGVKKPHRYRPGTVALREIRKYQKSTE  60
             MARTKQTARKSTGGKAPRKQLATKAARKSAPTTGGVKKPHRYRPGTVALREIRKYQKSTE
Sbjct:      1  MARTKQTARKSTGGKAPRKQLATKAARKSAPTTGGVKKPHRYRPGTVALREIRKYQKSTE  60
Histone H3  34  *****

Query:      61  LLIRKLPFQRLVREIAQDFKTDLRFAQSHAVLALQEAAEAYLVGLFEDTNLCAIHAKRVTI  120
             LLIRKLPFQRLVREIAQDFKTDLRFAQSHAVLALQEAAEAYLVGLFEDTNLCAIHAKRVTI
Sbjct:      61  LLIRKLPFQRLVREIAQDFKTDLRFAQSHAVLALQEAAEAYLVGLFEDTNLCAIHAKRVTI  120
Histone H3  61  *****

Query:      121 MPKDIQLARRIRGERA 136
             MPKDIQLARRIRGERA
Sbjct:      121 MPKDIQLARRIRGERA 136
Histone H3  121 *****
  
```

CPU time: 0.02 user secs. 0.01 sys. secs 0.03 total secs.

Lambda K H
 0.321 0.132 0.367

Gapped
 Lambda K H
 0.267 0.0410 0.140

Matrix: BLOSUM62
 Gap Penalties: Existence: 11, Extension: 1
 Number of Sequences: 1
 Number of Hits to DB: 284
 Number of extensions: 94
 Number of successful extensions: 1
 Number of sequences better than 10.0: 1



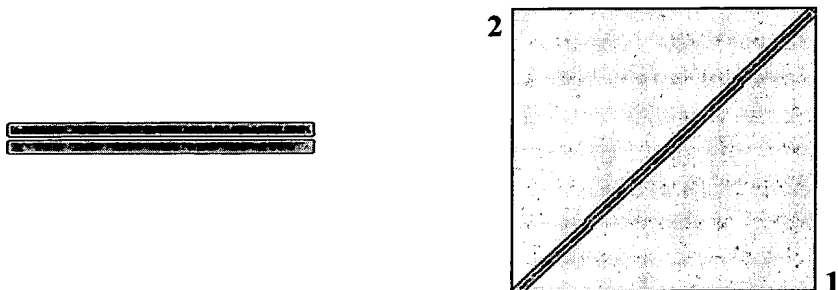
Blast 2 Sequences results

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BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.9 [May-01-2004]

Matrix: **BLOSUM62** gap open: **11** gap extension: **1**
x_dropoff: **50** expect: **10.000** wordsize: **3** Filter ☒ Align

Sequence 1 gi 16324 histone H3.3 like protein [Arabidopsis thaliana] Length 136 (1 .. 136)
Sequence 2 gi 42541263 putative histone H3 [Oryza sativa (japonica cultivar-group)] Length 136 (1 .. 136)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 266 bits (679), Expect = 1e-70
Identities = 136/136 (100%), Positives = 136/136 (100%)

```
Query:      1  MARTKQTARKSTGGKAPRKQLATKAARKSAPTTGGVKKPHRYRPGTVALREIRKYQKSTE 60
             MARTKQTARKSTGGKAPRKQLATKAARKSAPTTGGVKKPHRYRPGTVALREIRKYQKSTE
Sbjct:      1  MARTKQTARKSTGGKAPRKQLATKAARKSAPTTGGVKKPHRYRPGTVALREIRKYQKSTE 60
Histone H3 34  *****

Query:      61  LLIRKLPFQRLVREIAQDFKTDLRFSHAVLALQEAAEAYLVGLFEDTNLCAIHAKRVTI 120
             LLIRKLPFQRLVREIAQDFKTDLRFSHAVLALQEAAEAYLVGLFEDTNLCAIHAKRVTI
Sbjct:      61  LLIRKLPFQRLVREIAQDFKTDLRFSHAVLALQEAAEAYLVGLFEDTNLCAIHAKRVTI 120
Histone H3 61  *****

Query:      121 MPKDIQLARRIRGERA 136
             MPKDIQLARRIRGERA
Sbjct:      121 MPKDIQLARRIRGERA 136
Histone H3 121 *****
```

CPU time: 0.01 user secs. 0.00 sys. secs 0.01 total secs.

Lambda	K	H
0.321	0.132	0.367

Gapped Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
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